

## FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGGCTGCTAGGCCTC  
TGTGCCCCGGGCTTGGAATTCGGTGCGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT  
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCGGC  
GTTTGGCCCAGGACGGGGCCCATGTGGTCGTGAGCAGCCGGAAGCAGCAGAATGTGGACCAG  
GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA  
GGCGGAGGACCGGGAGCGGCTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC  
TAGTCTCCAATGCTGCTGTCAACCCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG  
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC  
AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCCATAGCAGCCTTCAGTC  
CATCTCCTGGCTTCAGTCCTTACAATGTCAGTAAAACAGCCTTGCTGGGCCTGACCAAGACC  
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAAGTGCCTAGCACCTGGACTTATCAA  
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC  
TGCGGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTTCCTGTGCTCT  
GAAGATGCCAGCTACATCACTGGGGAAACAGTGGTGGTGGGTGGAGGAACCCCGTCCCGCCT  
CTGAGGACCGGGAGACAGCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGCTGTTTCCTGC  
ATTCACCCACTGGCCTTTCCACCTCTGCTCACCTTACTGTTACCTCATCAAATCAGTTCT  
GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGTCTTACTCGGGATTCTCTGCT  
GTTGTTGTGGCCTTGGGTAAAGGCCTCCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT  
GAGTCTACCTTGGCAAAGACCAAGATATTTTTTCTGGGCCACTGGTGAATCTGAGGGGTGA  
TGGGAGAGAAGGAACCTGGAGTGAAGGAGCAGAGTTGCAAATTAACAGCTTGCAAATGAGG  
TGCAAATAAAATGCAGATGATTGCGCGGCTTTGAAAAAAAAA

095250-4095860

## FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672

><subunit 1 of 1, 278 aa, 1 stop

><MW: 29537, pI: 8.97, NX(S/T): 1

MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVS  
SRKQQNVVDQAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG  
SIMDVTEEVWDKTLTDINVKAPALMTKAVVPEMEKRGGSVVIVSSIAAFSPSPGFSPYNVSK  
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDC  
AGIVSFLCEDASYITGETVVVGGGTPSRL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation site.**

amino acids 183-186

**N-myristoylation sites.**

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 276-278

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# FIGURE 3

GCGCCCTGAGCTCCGCCTCCGGGCCCCGATAGCGGCATCGAGAGCGCCTCCGTCGAGGACCAGGCGGCG  
CAGGGGGCCGGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCCTGCAGAACCAGGTGGC  
GCGGCTGGAGGAGGAGAACCAGACTTTCTGGCTGCGCTGGAGGACGCCATGGAGCAGTACAACTGC  
AGAGCGACCGGCTGCGTGAGCAGCAGGAGGAGATGGTGGAACTGCGGCTGCGGTTAGAGCTGGTGGG  
CCAGGCTGGGGGGCCCTGCGGCTCCTGAATGGCCTGCCCTCCCGGGTCCTTTGTGCCTCGACCTCATAC  
AGCCCCCTGGGGGGTGCCACGCCCATGTGCTGGGCATGGTGCCGCTGCCTGCCTCCCTGGAGATG  
AAGTTGGCTCTGAGCAGAGGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT  
GAGGTGAACAGGCTGGGAAGTGGCTCTTCAGCTGCTTCAGAGGAGGAAGAGGAGGAGGAGGAGCCGCC  
CAGGCGGACCTTACACCTGCGCAGAAATAGGATCAGCAACTGCAGTCAGAGGGCGGGGGCACGCCCAG  
GGAGTCTGCCAGAGAGGAAGGGCCCAGAGCTTTGCCCTGAGGAGTTGGATGCAGCCATTCCAGGGTCC  
AGAGCAGTTGGTGGGAGCAAGGCCCGAGTTCAGGCCCGCCAGGTCCCCCTGCCACAGCCTCAGAGTG  
GCGGCTGGCCCAGGCCCAGCAGAAGATCCGGGAGCTGGCTATCAACATCCGCATGAAGGAGGAGCTTA  
TTGGCGAGCTGGTCCGCACAGGAAAGGCAGCTCAGGCCCTGAACGCCAGCACAGCCAGCGTATCCGG  
GAGCTGGAGCAGGAGGCAGAGCAGGTGCGGGCCGAGCTGAGTGAAGGCCAGAGGCAGCTGCGGGAGCT  
CGAGGGCAAGGAGCTCCAGGATGCTGGCGAGCGGTCTCGGCTCCAGGAGTCCGCAGGAGGGTGCCTG  
CGGCCCAGAGCCAGGTGCAGGTGCTGAAGGAGAAGAAGCAGGCTACGGAGCGGCTGGTGTCACTGTCTG  
GCCCAGAGTGAGAAGCGACTGCAGGAGCTCGAGCGGAACGTGCAGCTCATGCGGCAGCAGAGGGACA  
GCTGCAGAGGCGGCTTCGCGAGGAGACGGAGCAGAAGCGGCGCCTGGAGGCAGAAATGAGCAAGCGGC  
AGCACCGCGTCAAGGAGCTGGAGCTGAAGCATGAGCAACAGCAGAAGATCCTGAAGATTAAGACGGAA  
GAGATCGCGGCCCTTCAGAGGAAGAGGCGCAGTGGCAGCAACGGCTCTGTGGTCAGCCTGGAACAGCA  
GCAGAAGATTGAGGAGCAGAAGAAGTGGCTGGACCAGGAGATGGAGAAGGTGCTACAGCAGCGGCGGG  
CGCTGGAGGAGCTGGGGGAGGAGCTCCACAAGCGGGAGGCCATCCTGGCCAAGAAGGAGGCCCTGATG  
CAGGAGAAGACGGGGCTGGAGAGCAAGCGCCTGAGATCCAGCCAGGCCCTCAACGAGGACATCGTGCG  
AGTGTCCAGCCGGCTGGAGCACCTGGAGAAGGAGCTGTCCGAGAAGAGCGGGCAGCTGCGGCAGGGCA  
GCGCCCAGAGCCAGCAGCAGATCCGCGGGGAGATCGACAGCCTGCGCCAGGAGAAGGACTCGCTGCTC  
AAGCAGCGCCTGGAGATCGACGGCAAGCTGAGGCAGGGGAGTCTGCTGTCCCCGAGGAGGAGCGGAC  
GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGAATGAGGCCATCA  
CATGCCGCCAGCGGGTGCTTCGGGCCTCAGCCTCGTTGCTGTCCAGTGCGAGATGAACCTCATGGCC  
AAGCTCAGCTACCTCTCATCCTCAGAGACCAGAGCCCTCCTCTGCAAGTATTTTGACAAGGTGGTGAC  
GCTCCGAGAGGAGCAGCACCAGCAGCAGATTGCCCTTCTCGGAACTGGAGATGCAGCTGGAGGAGCAGC  
AGAGGCTGGTGTACTGGCTGGAGGTGGCCCTGGAGCGGCAGCGCCTGGAGATGGACCGCCAGCTGACC  
CTGCAGCAGAAGGAGCACGAGCAGAACATGCAGCTGCTCCTGCAGCAGAGTCGAGACACCTCGGTGA  
AGGGTTAGCAGACAGCAGGAGGCAGTATGAGGCCCGGATTCAAGCTCTGGAGAAGGAACCTGGGCCGTT  
ACATGTGGATAAACCAGGAACCTGAAACAGAAGCTCGGCGGTGTGAACGCTGTAGGCCACAGCAGGGGT  
GGGAGAAGAGGAGCCTGTGCTCGGAGGGCAGACAGGCTCCTGGAAATGAAGATGAGCTCCACCTGGC  
ACCCGAGCTTCTCTGGCTGTCCCCCTCACTGAGGGGGCCCCCGCACCCGGGAGGAGACGCGGGACT  
TGGTCCACGCTCCGTTACCTTGACCTGGAACGCTCGAGCCTGTGTGGTGAGGAGCAGGGGTCCCCC  
GAGGAACTGAGGCAGCGGGAGGCGGCTGAGCCCCCTGGTGGGGCGGGTGCTTCCTGTGGGTGAGGCAGG  
CCTGCCCTGGAACCTTGGGCCTTTGTCCAAGCCCCGGCGGGAACCTGCGACGAGCCAGCCCGGGGATGA  
TTGATGTCCGGAAAAACCCCTGTAAAGCCCTCGGGGCAGACCCTGCCTTGGAGGGAGACTCCGAGCCT  
GCTGAAAGGGGCAGCTGCCTGTTTGTCTTCTGTGAAGGGCAGTCCTTACCGCACACCCTAAATCCAGG  
CCCTCATCTGTACCCTCACTGGGATCAACAAATTTGGGCCATGGCCAAAAGAACTGGACCCTCATTT  
AACAAAATAATATGCAAAATCCCACCACTTACTTCCATGAAGCTGTGGTACCCAATTGCCGCCTTGTG  
TCTTGCTCGAATCTCAGGACAATTCTGGTTTCAGGCGTAAATGGATGTGCTTGTAGTTTCAGGGGTTTG  
GCCAAGAATCATCAGAAAGGGTCGGTGGCAACCAGGTTGTGGTTTAAATGGTCTTATGTATATAGGG  
GAACTGGGAGACTTTAGGATCTTAAAAAACCATTTAATAAAAAAAATCTTTGAAGGGAC

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## FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

MEQYKLQSDRLREQQEEMVELRLRLELVRPGWGGLRLLNGLPPGSFVVRPHTAPLGGAHAHV  
LGMVPPACLPQDEVGSEQRGEQVTNGREAGAELLTEVNRLGSGSSAASEEEEEEEPPRRTL  
HLRRNRISNCSQRAGARPGSLPERKGPCLCLEELDAAIPGSRAVGGSKARVQARQVPPATAS  
EWRLAQAAQQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE  
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQVLKEKKQATERLVSLSAQSEKRLQE  
LERNVQLMRQQQGQLQRRRLREETEQRRLLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA  
AFQKRKRRSGSNGSVVSLEQQQKIEEQKKWLDQEMEKVLQORRALEELGEELHKREAILAKKE  
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAAQSQQQIRGEIDS  
LRQEKDSLLKQRLEIDGKLRQGSLLSPEEERTLQFQLEAIEALDAAIEYKNEAITCRQRVLR  
ASASLLSQCEMNLMAKLSYLSSETRALLCKYFDKVVTLREEQHQQQIAFSELEMQLEEQQR  
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLLQQSRDHLGEGGLADSRQYEARIQALEK  
ELGRYMWINQELKQKLGGVNAVGHSGGKRSKLCSEGRQAPGNEDELHLAPELLWLSPLTEG  
APRTREETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG  
PLSKPRRELRRASPGMIDVRKNPL

### **Important features:**

#### **Leucine zipper pattern.**

amino acids 557-579, 794-815

#### **N-glycosylation sites.**

amino acids 133-136, 383-386

#### **Kinesin related protein Kif-4 Coiled-coil domain:**

amino acids 231-672

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## FIGURE 5

ATTCTCCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT  
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA  
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCTTCAGAGCAGTG  
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT  
TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTGTG  
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACCTTATCTCCCATCTCCCGGAGCTGTAC  
CAGGAACAGGAGGCACGTCCTGTACCCATTAAAAACCCAGGCTCCACTGGCAGACGGCAGAC  
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA  
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCCAGCTGGGGATGGC  
CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCTTTCCAGCTCCCCTTCCCGCTGAG  
AGCCACTTTCATCGGCAATAAAATCCCCCACATTTACCATCT

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105250-4E09860

## FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700

><subunit 1 of 1, 125 aa, 1 stop

><MW: 14198, pI: 9.01, NX(S/T): 1

MRPRCCILALVCWITVFLQCSKGTTDAPVGSGLWLCQPTPRCGNKIYNPSEQCCYDDAILS  
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISRCTRNRHVLYP

**Important features:**

**Signal sequence**

amino acids 1-21

**N-myristoylation sites.**

amino acids 33-39, 70-76

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## FIGURE 7

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCT  
TTTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG  
AACCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCG  
GAGAAGCGGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT  
GGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCCG  
GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTAGTGGTCCGCCCCACGCGGG  
TCGCCGGCCGGCCCAGGATGGGCGCTGGCAACCCGGGGCCGCGCCCGCCGCTGCTACCCCTG  
CGCCCGCTGCGAGCCCGGCGTCCGGCCCCGCGCCCTGCGCTCATGGACGGCGGGCTCCCGGCTG  
GCGGCGGCGCGCCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGCCGCGCTCCCCGCCCGCCC  
GCCCGCCGGGACGTGGTAGGGGATGCCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA  
GTTCCCTCCTGGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAG  
AAGCTGGCCCAGGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGG  
CCCGGGGCGGGTGAACGAGCTCGGGCGCCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACT  
GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC  
TGGGTCTCCCAGGGCGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACAC  
CCCGCAGGCGGAAGCCCTGGCCGAGCCGCCAGGACGCGATTGGCCCGGAACCTCGCGCCCA  
CGCCCCGAGCCACCCGAGGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAG  
AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTCGCGCCGGGCCCCCTCGGCCTGCCCGTGCCT  
GTGCACCGAGGAGGGGCCGCTGTGCGCGCAGCCCGAGTGCCCGAGGCTGCACCCGCGCTGCA  
TCCACGTCGACACGAGCCAGTGCTGCCCCGAGTGCAAGGAGAGGAAGAACTACTGCGAGTTC  
CGGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTGCTG  
TGAAGCCAACGGTGAGGTGCTATGCACAGTGTGAGCGTGTCCCCAGACGGAGTGTGTGGACC  
CTGTGTACGAGCCTGATCAGTGCTGTCCCATCTGCAAAAATGGTCCAAACTGCTTTGCAGAA  
ACCGCGGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGACCATATGCCACTGTAC  
TTATGAGGAAGGCACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC  
AAATGTAGACGCTTCCCAGAACACAACTCTGACTTTTTCTAGAACATTTTACTGATGTGAA  
CATTCTAGATGACTCTGGGAACCTATCAGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAA  
TTGTTGGTACTTTTCTTTCTTGATAACAGTTACTACAACAGAAGGAAATGGATATATTTT  
AAAACATCAACAAGAACTTTGGGCATAAAATCCTTCTCTAAATAAATGTGCTATTTTCACAG  
TAAGTACACAAAAGTACACTATTATATATCAAATGTATTTCTATAATCCCTCCATTAGAGAG  
CTTATATAAGTGTTTTCTATAGATGCAGATTAAAAATGCTGTGTTGTCAACCGTCAAAAAA  
AAAAAAAAAAAAAAAAAAAA

0966034.052501

## **FIGURE 8**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818

><subunit 1 of 1, 325 aa, 1 stop

><MW: 35296, pI: 5.37, NX(S/T): 0

MPSSTAMAVGALSSSLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNEL  
GRPARDEGGSGRDWKS KSGRGLAGREPWSK LKQAWVSQGGGAKAGDLQVRPRG DTPQAEALA  
AAAQDAIGPELAPTPEPP EYVYPDYRGKGCVDESGFVYAIG EKFA PGPSACPC LCTEEGPL  
CAQPEC PRLHPRCIHV DTSQCCPQCK ERKNYCEFRGKTYQTLEEFV VSPCERCRCEANGEVL  
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVK TDECTICHCTYE EGTWR  
IERQAMCTRHECRQM

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-27

#### **Transmembrane domain:**

amino acids 11-30

#### **Glycosaminoglycan attachment site.**

amino acids 80-83

#### **N-myristoylation sites.**

amino acids 10-15, 102-107, 103-108

#### **Cell attachment sequence.**

amino acids 114-117

#### **EGF-like domain cysteine pattern signature.**

amino acids 176-187

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## FIGURE 9

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC  
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC  
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA  
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG  
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC  
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT  
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG  
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT  
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC  
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCTGGGTATGACTGAGA  
ACTGCAATAGGAAAGATTTTCTGACCTGTATCGGGGGACCACCATTATGACACACGGAAAC  
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT  
GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG  
GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG  
GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG  
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCGTGCCAGGAGACCGGCAGTGTC  
CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG  
GGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAT  
GAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCG  
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT  
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG  
GTGGGGAGTGGTTTGCCCTTCCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA  
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC  
CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTATCTACTCACCTAACAGCA  
AACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG  
GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

0986034.052501

## **FIGURE 10**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847

><subunit 1 of 1, 437 aa, 1 stop

><MW: 46363, pI: 6.22, NX(S/T): 3

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI  
ESGPQVSLVLKSGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP  
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTCHYDGLLRGRGGIFSNLRVQGCMPQPGCN  
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSENTEMCEVGQVCQETL  
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN  
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC  
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGVGLALAPALWWGVVCPSC

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-15

#### **Transmembrane domain:**

amino acids 243-260

#### **N-glycosylation sites.**

amino acids 46-49, 189-192, 382-385

#### **Glycosaminoglycan attachment sites.**

amino acids 51-54, 359-362

#### **N-myristoylation sites.**

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,  
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,  
360-365, 361-366, 388-393, 408-413, 419-424

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# FIGURE 11

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTG  
GCTGCGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGGC  
CTCGTCGCTCAGCCCCCTATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTAT  
TGTCGGGCCCCGAGGCTCCGTGGCGGGACCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTG  
CAGCTGGTCGCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCT  
GAGGCAGCTGCACGGGTGCTGTCAGGCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCG  
GCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGAC  
GGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCT  
CTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCGCTGCGGCTCATCACCAGTTCOAAGC  
ACCGCTGCATGGATAGCAGCGCCGCTTCTGTCAGGGGCTGTGGCAGCACTACCACCCTGGC  
TTGCCGCCGCCGGACGTGCGAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAAT  
GAGATTTTTTGTATCACTGTGAGAAGTTTTTAACTGAAGTAGAAAAAATGCTACAGCTCTTT  
ATCACGTGGAAGCCTTCAAACTGGACCAGAAATGCAGAACATTTTTAAAAAAGTTGCAGCT  
ACTTTGCAAGTGCCAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTTACCTG  
TTCATTTGACCTGGCAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGCATAGATG  
ATGCAAAGGTATTAGAATATTTAAATGATCTGAAACAATATTGGAAAAGAGGATATGGGTAT  
ACTATTAACAGTCGATCCAGCTGCACCTTGTTTTAGGATATCTTTCAGCACTTGGACAAAGC  
AGTTGAACAGAAACAAAGGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATG  
CAGAGACTCTTCTTCCACTGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACA  
GCGTACAATTACAAAAACAAATGCATCGGAAGTTCCGAAGTGGTCTCATTGTACCTTATGC  
CTCGAACCTGATATTTGTGCTTTACCACTGTGAAAATGCTAAGACTCCTAAAGAACAAATTC  
GAGTGCAGATGTTATTAAATGAAAAGGTGTTACCTTTGGCTTACTCACAAGAACTGTTTCA  
TTTTATGAAGATCTGAAGAACCCTACAAGGACATCCTTCAGAGTTGTCAAACCAGTGAAGA  
ATGTGAATTAGCAAGGGCTAACAGTACATCTGATGAACTATGAGTAACTGAAGAACATTTTT  
AATTCTTTAGGAATCTGCAATGAGTGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATT  
ACAGGAAGCTTTTATATTACTTGAGTATTTCTGTCTTTTACAGAAAAACATTGGGTTTCTC  
TCTGGGTTTGGACATGAAATGTAAGAAAAGATTTTTTCACTGGAGCAGCTCTCTTAAGGAGAA  
ACAAATCTATTTAGAGAAACAGCTGGCCCTGCAAATGTTTACAGAAATGAAATTCTTCCTAC  
TTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTTATAATAACACTTGAAAAGTGCT  
GGAGTAACAAAATATCTCAGTTGGACCATCCTTAACTTGATTGAACTGTCTAGGAACCTTAC  
AGATTGTTCTGCAGTTCTCTCTTTTCTTCTCAGGTAGGACAGCTCTAGCATTTTCTTAATC  
AGGAATATTGTGGTAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGAGAAT  
TTGAAACAAGAAACAGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGGAAAGTACAA  
TGAAAATAAATATTTTTTGGTATTTATTTATGAAATATTTGAACATTTTTTCAATAATTCCTT  
TTTACTTCTAGGAAGTCTCAAAGACCATCTTAAATTATTATATGTTTGGACAATTAGCAAC  
AAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACTTTTTTCATTCTGT  
CACTTGGCTTCGATTTTTTATATTTTCTATTATATGAAATGTATCTTTTGGTTGTTTGATTT  
TTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAA  
TAAAGAAAATTCCTGTGACTTTAAAAA

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## FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76400

><subunit 1 of 1, 487 aa, 1 stop

><MW: 55051, pI: 8.14, NX(S/T): 2

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSFYFGTKTRYEDVNPVLLS  
GPEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGS  
RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR  
CMDSSAAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH  
VEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSFDLAIKGVKSPWCDVFDIDDA  
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE  
TLLPLLSLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV  
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

### **Important features:**

#### **Signal sequence**

amino acids 1-30

#### **N-glycosylation sites.**

amino acids 242-246, 481-485

#### **N-myristoylation sites.**

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

#### **Endoplasmic reticulum targeting sequence.**

amino acids 484-489

09866034-052501

## FIGURE 13

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAAGTGTCTTGCATCATTACGGATTTCGC  
AGACAAGTGACCCCAGGATCGAGTGGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTTTTGACAACAAAA  
TTCAGGGGAGACTTGGCGGGTTCGTGCAGAAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTTATCGCTGTGAGGTTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT  
CCAGAGCCAATCCCAGATTTTCGCAATTCTTCTTTCCACTTAAACTCTGAAACAGGCACCTTTGGTGTTCCTGCTG  
TTCACAAGGACGACTCTGGGCGAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTGTCTTGTCTGACTGGCCCTGA  
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAACAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG  
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCCTAATCTGTTTTCTGGCCTGATTCCCGCATGAGTATTAGG  
GTGATCTTAAAGAGTTTGCTCACGTAAACGCCCGTGTGGGCCCTGTGAAGCCAGCATGTTCACTGCTGGTTCGTT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGGCGGGAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG  
GTAAATTGGTTGCTGGAAGAGGGATCTTGCTGAGGAACCTGCTTGTCCAACAGGTGTGAGGATTAAAGGAAA  
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTT  
TACATCTAAATTTTGCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAAACTGTAAATATATTGT  
CATACAATGTTAAATAACCTATTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT  
TGGAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTTTTCT  
CACACAAGTTTTCAGCTTTTTCACAAGGGAACCTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATTCCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAAACCTCTCAGGTTAGCTTTGAACT  
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG  
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCTCGCTGCTGCCAGGAGGCCCT  
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAACAGACCTCT  
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTAAAGTTGTTTAAATATTTGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTAAAAGAAAATGGAT  
CCCCTGTTCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACTGAGGTGGAGCAGCCAGGTGAAAGGCTGGCGGGGAGGAAAG  
TGAAACGCCTGAATCAAAAGCAGTTTCTAATTTTGACTTTAAATTTTTCATCCGCCGAGACACTGCTCCCATT  
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGA  
GAATGGCTCTCACTACTCACCTTGTCTTTAGCTTCCAGTGTCTTGGGTTTTTTTATCTTTGACAGCTTTTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTTTTAGTTATGTGAAACACTTTGCCGAGGCCGCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACAGCTCCAGCCTCCT  
TCTTGGTTGTCATAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAAACTTCTACACTAGTGCCA  
TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTGTTTAAAC  
CTCATTTATAAAAGCTTCAAAAAACCCA

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## FIGURE 14

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS  
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTS�KIWNVTRRDSALYRCEVVARNDRK  
EIDEIVIELTVQVKPVPVCRVPAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA  
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEYDLNIGGIIGG  
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-30

#### **Transmembrane domain:**

amino acids 243-263

#### **N-glycosylation sites.**

amino acids 104-107, 192-195

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

#### **Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

#### **Tyrosine kinase phosphorylation site.**

amino acids 69-77

#### **N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

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# FIGURE 15

CAGGACCAGGTCTTCTACGCTGGAGCAGCGGGGAGACAGCCACCATGCACATCCTCGTGGTCCATGCCATGGTG  
ATCCTGCTGACGCTGGGCCCCGCTCGAGCCGACGACAGCGAGTTCCAGGCGCTGCTGGACATCTGGTTTCCGGAG  
GAGAAGCCACTGCCCCACGCCTTCTGGTGGACACATCGGAGGAGGCGCTGCTGCTTCTGACTGGCTGAAGCTG  
CGCATGATCCGTTCTGAGGTGCTCCGCCGGTGGACGCCGCCCTGCAGGACCTGGAGCCGCAGCAGCTGCTGCTG  
TTCGTGCAGTCGTTTGGCATCCCCGTGTCCAGCATGAGCAAACCTCCTCCAGTTCTGAGACCAGGCAGTGGCCAC  
GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAATTACATGGCCCCACCTGGTGGAGGTCCAGCATGAGCGC  
GGCGCCTCCGGAGGCCAGACTTTCCACTCCTTGCTCACAGCCTCCCTGCCGCCCGCCGAGACAGCACAGAGGCA  
CCCAAACCAAAGAGCAGCCCAGAGCAGCCCATAGGCCAGGGCCGGATTTCGGGTGGGGACCCAGCTCCGGGTGCTG  
GGCCCTGAGGACGACCTGGCTGGCATGTTCTCCTCCAGATTTTCCCGCTCAGCCCGGACCCCTCGGTGGCAGAGCTCC  
AGTCCCCGCCCGCTGGCCCTCGCCCTGCAGCAGGCCCTGGGCCAGGAGCTGGCCCCGCTCGTCCAGGGCAGCCCC  
GAGGTGCCGGGCATCACGGTGCCTGCTGTCAGGCCCTCGCCACCCTGCTCAGCTCCCCACACGGCGGTGCCCTG  
GTGATGTCCATGCACCGTAGCCACTTCTGTCCTGCCCCGCTGCTGCGCCAGCTCTGCCAGTACCAGCGCTGTGTG  
CCACAGGACACCGGCTTCTCCTCGCTCTTCTGAAGGTGCTCCTGCAGATGCTGCAGTGGCTGGACAGCCCTGGC  
GTGGAGGGCGGGCCCCCTGCGGGCACAGCTCAGGATGCTTGCCAGCCAGGCCTCAGCCGGGCGCAGGCTCAGTGAT  
GTGCGAGGGGGGCTCCTGCGCCTGGCCGAGGCCCTGGCCTTCCGTGAGGACCTGGAGGTGGTCACTCCACCGTC  
CGTGCCGTATCGCCACCCTGAGGTCTGGGGAGCAGTGCAGCGTGGAGCCGGACCTGATCAGCAAAGTCTCTCCAG  
GGGCTGATCGAGGTGAGGTCCCCCACCTGGAGGAGCTGCTGACTGCATTCTTCTGCTGCTGCGGATGCTGCC  
TCCCCGTTTCCAGCCTGTAAGCCCGTGTGGTGGTGAGCTCCCTGCTGCTGTCAGGAGGAGGAGCCCCCTGGCTGGG  
GGGAAGCCGGGTGCGGACGGTGGCAGCCTGGAGGCCGTGCGGCTGGGGCCCCCTCGTCAGGCCCTCCTAGTGGACTGG  
CTGGAATGCTGGACCCCCGAGGTGGTCAAGCAGCTGCCCGACCTGCAGCTCAGGCTGCTTCTCTCCGGAGGAAG  
GGCAAAGGTGAGGCCAGGTGCCCTCGTTCGCTCCCTACCTCCTGACCCTCTTCACGCATCAGTCCAGCTGGCCC  
ACACTGCACCAAGTGCATCCGAGTCTGCTGGCAAGAGCCGGGAACAGAGGTTGACCCCTCTGCCTCTCTGGAC  
TTCCTCTGGGCTGCATCCATGTTCTCTCGCATCTGGCAGGGGCGGGACCAGCGCACCCCGCAGAAGCGGCGGGAG  
GAGCTGGTGCTGCGGGTCCAGGGCCCCGAGCTCATCAGCCTGGTGGAGCTGATCCTGGCCGAGGCGGAGACGCGG  
AGCCAGGACGGGGACACAGCCGCCCTGCAGCCTCATCCAGGCCCGGCTGCCCCCTGCTGCTCAGCTGCTGCTGTGGG  
GACGATGAGAGTGTGAGGAAGGTGACGGAGCACCTGTGAGGCTGCATCCAGCAGTGGGGAGACAGCGTGTGGGA  
AGGCGCTGCCGAGACCTTCTCCTGCAGCTCTACCTACAGCGGCCGAGCTGCGGGTGCCCGTGCTGAGGTCTTA  
CTGCACAGCGAAGGGGCTGCCAGCAGCAGCTCTGCAAGCTGGACGGACTCATCCACCGCTTCATCAGCTCCTT  
GCGGACACCAGCGACTCCCCGGCGTTGGAGAACCGAGGGGCGGATGCCAGCATGGCTGCCGGAAGCTGGCGGTG  
GCGCACCCGCTGCTGCTGCTCAGGCACCTGCCCATGATCGCGGCGCTCCTGCACGGCCGCACCCACCTCAACTTC  
CAGGAGTTCCGGCAGCAGAACCCACCTGAGCTGCTTCTGTCAGTGTGCTGGGCTGCTGGAGCTGCTGCAGCCGCAC  
GTGTTCCGAGCAGCAGCAGGAGGGGCGCTGTGGGACTGCCTTCTGTCTTCATCCGCTGCTGCTGAATTACAGG  
AAGTCTCCCCGCCATCTGGCTGCCTTCATCAACAAGTTTGTGTCAGTTTCATCCATAAGTACATTACCTACAATGCC  
CCAGCAGCCATCTCCTTCTGTCAGAACGACGCCGACCCGCTCCACGACCTGTCTTCGACAACAGTGACCTGGTG  
ATGCTGAAATCCCTCCTTGCAGGGCTCAGCCTGCCAGCAGGGACGACAGGACCGACCGAGGCCTGGACGAAGAG  
GGCGAGGAGGAGAGCTCAGCCGGCTCCTTGCCCCCTGGTCAAGCTCTCCCTGTTACCCCTCTGACCGCGGCCGAG  
ATGGCCCCCTACATGAAACGGCTTTCCCGGGGCCAAACGGTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC  
GAGATGTCCCGCGGAGACCCGAGATCCTGAGCTTCTTCTGACCAACCTGCAGCGGCTGATGAGCTCGGCCGAG  
GAGTGTGCGGCAACCTCGCCTTCAGCCTGGCCCTGCGCTCCATGCAGAACAGCCCCAGCATTGCAGCCGCTTTC  
CTGCCCACGTTTCATGTAAGTGGTGGCAGCCAGGACTTTGAGGTGGTGCAGACGGCCCTCCGGAACCTGCCTGAG  
TACGCTCTCCTGTGCCAAGAGCACGCGGCTGTGCTGCTCCACCGGGCCTTCTGGTGGGCATGTACGGCCAGATG  
GACCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATGGAGGCCGTGATGTGAGGCCTGTGGCAGCCGA  
CCCCCTCCAAGCCCCGCGCCGTCCCGTCCCCGGGGATCCTCGAGGCAAAGCCCCAGGAAGCGTGGGCGTTGCTGG  
TCTGTCCGAGGAGGTGAGGGCGCCGAGCCCTGAGGCCAGGCAGGCCAGGAGCAATACTCCGAGCCCTGGGGTGG  
CTCCGGGCGCGCGCTGGCATCAGGGGCCGTCCAGCAAGCCCTCATTCACCTTCTGGGCCACAGCCCTGCCGCGG  
AGCGGCGGATCCCCCGGCATGGCCTGGGCTGGTTTTGAATGAAACGACCTGAACTGTCAA

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## FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

MHILVVHAMVILLTLGPPRADDSEFQALLDIWFPEEKPLPTAFLVDTSEEALLLPDWLKLRM  
IRSEVLRLVDAALQDLEPQQQLLLFVQSFGIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNY  
MAHLVEVQHERGASGGQTFHSLLTASLPPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLG  
PEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL  
ATLLSSPHGGALVMSMRSHFLACPLLRLCQYQRCVPQDTGFSSFLKVLLQMLQWLDS PG  
VEGGPLRAQLRMLASQASAGRRLSDVRGLLRLAEALAFRQDLEVVSSTVRAVIATLRSGEQ  
CSVEPD LISKVLQGLIEVRSPHLEELLTAFFSATADAASPFPAKPVVVVSSLLLQEEEEPLA  
GGKPGADGGSLEAVRLGPSSGLLVDWLEMLDPEVVSSCPDLQLRLLFSRRKGKGQAQVPSFR  
PYLLTLFTHQSSWPTLHQCIQIRVLLGKSREQRFDPSASLDFLWACIHVPRIWQGRDQRTPOKR  
REELVLRVQGP ELISLVELILAEAE TRSQDGD TAACSLIQARLPLLLSCCCGDDESVRKVTE  
HLSGCIQQWGD SVLGRRCDLLQLYLQRP ELRVPVPEVLLHSEGAASSSVCKLDGLIHRFI  
TLLADTSDSRALENRGADASMACRKLAVAHPLLLLRHLPMIAALLHGRTHLNFQEFRQQNHL  
SCFLHVLGLLELLQPHVFRSEHQGALWDCLLSFIRLLLNRYKSSRHAAFINKFVQFIHKYI  
TYNAPAAISFLQKHADPLHDL SFDNSDLV MLKSLLAGLSLPSRDDRTDRGLDEEGEEESSAG  
SLPLVSVSLFTPLTAAEMAPYMKRLSRGQTVEDLLEVLSDIDEMSRRRPEILSFFSTNLQRL  
MSSAECCRNLAFLSLALRSMQNSPSIAAAFLPTFMYCLGSQDFEVVQTALRNLPEYALLCQE  
HAAVLLHRAFLVGMYGQMDPSAQISEALRILHMEAVM

### Important features:

#### Signal peptide:

amino acids 1-16

#### cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

#### N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,  
665-671, 698-704

#### Amidation sites.

amino acids 329-333, 634-638

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# FIGURE 17

CCGGGCCATGCAGCCTCGGCCCCGCGGGCGCCCCGCCGCGCACCCGAGGAGATGAGGCTCCGC  
AATGGCACCTTCTGACGCTGCTGCTCTTCTGCCTGTGCGCCTTCTCTCGCTGTCCTGGTA  
CGCGGCACTCAGCGGCCAGAAAGGCGACGTTGTGGACGTTTACCAGCGGGAGTTCCTGGCGC  
TGCGCGATCGGTTGCACGCAGCTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTCAACCTG  
GTGCTGGACGAGATCAAGAGGGCCGTGTGAGAAAGGCAGGCGCTGCGAGACGGAGACGGCAA  
TCGCACCTGGGGCCGCTAACAGAGGACCCCCGATTGAAGCCGTGGAACGGCTCACACCGGC  
ACGTGCTGCACCTGCCCACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGT  
CTGCAGCCCCGCGGTGCGCGTGGGCCAGGGCCGCACCGGAGTGTGCGGTGGTGATGGGCATCCC  
GAGCGTGCGGCGCGAGGTGCACTCGTACCTGACTGACACTCTGCACTCGCTCATCTCCGAGC  
TGAGCCCGCAGGAGAAGGAGGACTCGGTCATCGTGGTGCTGATCGCCGAGACTGACTCACAG  
TACACTTCGGCAGTGACAGAGAACATCAAGGCCTTGTTCCCCACGGAGATCCATTCTGGGCT  
CCTGGAGGTCATCTCACCTCCCCCACTTCTACCTGACTTCTCCCGCCTCCGAGAGTCCT  
TTGGGGACCCCAAGGAGAGAGTCAGGTGGAGGACAAACAGAACCTCGATTACTGCTTCCTC  
ATGATGTACGCGCAGTCCAAAGGCATCTACTACGTGCAGCTGGAGGATGACATCGTGGCCAA  
GCCCCAATACTGAGCACCATGAAGAACTTTGCACTGCAGCAGCCTTCAGAGGACTGGATGA  
TCCTGGAGTTCTCCCAGCTGGGCTTCATTGGTAAGATGTTCAAGTCGCTGGACCTGAGCCTG  
ATTGTAGAGTTCATTCTCATGTTCTACCGGGACAAGCCCATCGACTGGCTCCTGGACCATAT  
TCTGTGGGTGAAAGTCTGCAACCCCCGAGAAGGATGCGAAGCACTGTGACCGGCAGAAAGCCA  
ACCTGCGGATCCGCTTCAAACCGTCCCTCTTCCAGCACGTGGGCACTCACTCCTCGCTGGCT  
GGCAAGATCCAGAACTGAAGGACAAAGACTTTGGAAAGCAGGCGCTGCGGAAGGAGCATGT  
GAACCCGCCAGCAGAGGTGAGCACGAGCCTGAAGACATAACAGCACTTCACCCTGGAGAAAG  
CCTACCTGCGCGAGGACTTCTTCTGGGCCTTCACCCCTGCCGCGGGGGACTTCATCCGCTTC  
CGCTTCTTCCAACCTCTAAGACTGGAGCGGTTCTTCTTCCGCAGTGGGAACATCGAGCACC  
GGAGGACAAGCTCTTCAACACGTCTGTGGAGGTGCTGCCCTTCGACAACCCTCAGTCAGACA  
AGGAGGCCCTGCAGGAGGGCCGCACCGCCACCCTCCGGTACCCTCGGAGCCCCGACGGCTAC  
CTCCAGATCGGCTCCTTCTACAAGGGAGTGGCAGAGGGAGAGGTGGACCCAGCCTTCGGCCC  
TCTGGAAGCACTGCGCCTCTCGATCCAGACGGACTCCCCTGTGTGGGTGATTCTGAGCGAGA  
TCTTCCTGAAAAAGGCCGACTAAGCTGCGGGCTTCTGAGGGTACCCTGTGGCCAGCCCTGAA  
GCCCACATTTCTGGGGGTGTCGTCACTGCCGTCCCCGGAGGGCCAGATACGGCCCCGCCAA  
AGGGTTCTGCCTGGCGTCCGGCTTGGGCCGGCCTGGGGTCCGCCGCTGGCCCCGGAGGCCCTA  
GGAGCTGGTGCTGCCCCCGCCCGCCGGGCCGCGGAGGAGGCAGGCGGCCCCCACACTGTGCC  
TGAGGCCCCGAACCGTTTCGCACCCGGCCTGCCCCAGTCAGGCCGTTTTAGAAGAGCTTTTAC  
TTGGGCGCCCCGCGTCTCTGGCGCGAACACTGGAATGCATATACTACTTTATGTGCTGTGTT  
TTTTATTCTTGATACATTTGATTTTTTTCACGTAAGTCCACATATACTTCTATAAGAGCGTG  
ACTTGTAATAAAGGTTAATGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

09866034.052501

## FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307

><subunit 1 of 1, 548 aa, 1 stop

><MW: 63198, pI: 8.10, NX(S/T): 4

MRLRNGTFLTLLLFCLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDR LHAAEQESLKRSK  
ELNLVLDEIKRAVSERQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLA  
KESSLQPAVRVGQGRTGVSVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLIAE  
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRLRESFGDPKERVWRWTKQNLD  
YCFLMMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL  
DLSSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGT  
HSSLAGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDDFFWAFTPAAGD  
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLPFDNPQSDKEALQEGRTATLRYPRS  
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTDSPVWVILSEIFLKKAD

### **Important features:**

#### **Signal sequence**

amino acids 1-23

#### **N-glycosylation sites.**

amino acids 5-9, 87-91, 103-107, 465-469

#### **N-myristoylation sites.**

amino acids 6-12, 136-142, 370-376, 509-515

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